10

15 That and how that wife

20]

25

30

- (1) GENERAL INFORMATION:
 - (iii) NUMBER OF SEQUENCES: 23
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6689 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic) human
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION: 17p13.1
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ggcctcccaa agtgctggat tacaggcgtg agtcaccgcg cctggtcccc tgtcttcttt

aagaaagctc agcggacctt tttccttctt ggggtggaac aaaaagccaa atctagcaca 121

accetgggca ggggcccaga atcactggaa gcaaaggtgg atgggatagg aggcgaggct 181

gcctgtggac cacaggcccg gcccgagtgg ctctgatgag aagccggggc gcctaggtca 241

ccgccccac cgtctgcct tcccccact cctcctggct gggtaaatcc cagagtctca 301

geogectaag tgtcttcccc ggaggtgaga ttatctccgc ctgtgctgga cacctccctt 361

tctcctgcag ccatggatgc cgctctgctc ctgaacgtgg aaggggtcaa gaaaaccatt
421

ctgcacgggg gcacgggcga gctcccaaac ttcatcaccg gatcccgagt gagtggggcc 481

cctccggagc agacagggtc ccccacagca gctttcaaca ttccaggtgt gccccaaggc

	541					
	actgtaaaca	gctttcagct	gtgccaaaaa	aacagccagg	cagccccagc	gctgggcctc
	601					
	cggggagctc	ccagcgttta	cccattcagg	gggcattttt	ggtactttgc	agattcaact
5	661					
		ctgaggggaa	gggcttttgg	gaattttctg	gggccctaaa	tgttgagtga
	721					
		agtccgagga	gtcttggtat	ttgtccccaa	atgtctgtta	ggcttccctg
10	781					
10		tgcgtctgtg	gctacagaat	tegggetttg	gccaggcgag	geggeteeeg
	841				~~+ ~~ ~~+ ~~	2000++0020
		cagcactttg	ggaggccaag	atgggcagat	catgaggtca	agagetegag
417 7000	901	aaaaaatata	222444	tataataaaa	2+2422222+	tagggagatg
1		ccaacatgtg	adaccccatc	tetaetgaaa	atacaaaaat	tayccayacy
15 ⁰	961	aatataataa	gagttgagat	agtgaggaga	cttaaaacaa	gagaatgagt
	1021	Cotycaacoo	Cagcccagac	acccayyaya	cttgaggcag	gagaaccacc
And the second of the second o		aggtggaggt	tacaataaac	cgagatcata	ccactgcact	ccaacctggg
See	1081	<u> </u>	cgcagcgagc	ogagaooaoa	000.00	
20		agactctgtc	tcaqaaaaaa	aaaaaaaaaa	aagaactcgg	gcttacttga
ş. nibe	1141	5 5	J		3 33	
		ctqqacqcac	agggctgtgg	ggagtggaat	ggggtctgta	gggaggggtg
The second secon	1201					
To 1 a supplier	ggtccctcct	ccctgggggg	tgcaggcagg	gtggaggtgc	tccaggggtc	tgaggcatct
25	1261					
	gatggggtga	actgagtgag	ctgaccctgg	ggacagccct	gggtgtcggt	ggcaaggggg
	1321					
	tggcttctgc	cgggccttga	acagtgtgtc	tagagcagag	tgcaccgtct	cggtgactag
	1381					
30	gtgatctttc	atttccgcac	catgaaatgt	gatgaggagc	ggacagtcat	tgacgacagt
	1441					
	cggcaggtgg	gccagcccat	gcacatcatc	atcggaaaca	tgttcaagct	cgaggtctgg
	1501					
	gagatectge	ttacctccat	acaaatacac	gaggtggccg	agttctggtg	cgacaccatc

	1561					
	gtaagtaggc	cctgcgcgcc	tgtctcctgg	gactagtctt	ttctgggctc	acccacccgc
	1621					
	tttgcggggc	tgctgtgttt	cgggaaagct	gggactcaag	cgaagctttg	caaagccagt
5	1681					
	cctgcaaact	tattccccac	cgtgtgcatg	tgaagatgga	gggaacaagg	gctggaaggg
	1741					
	gtgacccatg	ctgtggctgg	ctggtgggga	gcagggctat	gaccagcagg	agtgagctgg
	1801					
10	cccacttcac	agtcctcaca	tctgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg
	1861					
	tgtgtgtgtg	agagagagag	agagagagag	agagagnnnn	nnnnnntagc	cttaggactt
	1921					
		ccaacaccta	acaatgtaat	caggcagcca	gtgcaggaca	taaataagta
15	1981					
AND METALL STATE OF THE STATE O		ctttgggcca	caaaagcacg	ctcagcttgc	tggaagccat	gggtgccgag
All hands	2041					~~++ a+ aaaa
		ctgagtcagg	gccaaagggg	gecectecet	gcagtaagct	ggrrergggg
N	2101			aan aan aa aa a	annanagant	ataattatat
201		ccttggtcca	getettaate	CCaacaggct	caacagccat	diguitgue
14 4.1	2161	~~~~~~~~	agatttaggg	ataataaaa	ccaataaaa	aaacaaaata
	2221	gaggcagaag	geattteggg	ctaatcccgg	ccggtggggc	3930033303
To SE CONTROL OF THE PROPERTY		ctatactaat	gacctggagg	cagagetgaa	ctgctgcata	gagtttcagc
25	2281		3400033433			JJ J
		cacatqttqc	atatagaacc	agtgctgggt	catctcagaa	gccggtccaa
	2341		5 5555	3 3 333	· ·	
	ggagatgggt	tctcagggag	cctagttggg	gaaactgagg	cccagcatac	atacagcagg
	2401					
30	cctcgctgag	gccgcacggc	ggatcttccc	agccctcctt	catcccaagg	gtggcaaact
	2461					
	cagctcccat	gctggctgaa	gctgtgatga	gccagatcta	tatctgcacc	atctcattta
	2521					
	atccctacaq	caqccctaat	atcqaacaqq	agcaacccag	ggaactgagt	ttcagagaag

	2581					
	tgcagagacc	tgggctcacc	gctaacctgc	agcactgcca	ggacaccaaa	gcgactctct
	2641					
	tggaccctgg	agtcctgctc	cttctactgc	cccacactgc	ccttcctgcg	agtcataggc
5	2701					
	tttgcagagg	tcagggtttc	cctggggcag	agatgtgtta	cagtggacca	caagggccag
	2761					
	aagaggcagc	cggaggctaa	cagcatatgg	cctctggagc	caggtttgaa	tcctggctgc
	2821					
10	gtcatttcct	agctgtgtga	ccttaagcaa	gttgcttgcg	tctctgggct	gtagtttccc
	2881					
	catccgtaaa	atgggataat	agtgcctgcc	ttgaattgtc	ataaggattg	aaggggctca
	2941					
and mining	taacagtgtg	aagtgctttg	cctggcacac	agttaaccac	agttagtatg	agtggcatag
15	3001					
1 SE CAMPA 12 LA SEGUENT W 15 LA SEGUENT W 15 LA SEGUENT W 15 LA SEGUENT 10	tgagggagca	ggattcctcc	caggaggggc	tctgagtgga	ggccttttat	ggcccaccta
A CONTRACTOR OF THE CONTRACTOR	3061					
		ggtagcctgg	atgccatcca	tccgtttatc	cccacagcac	acgggggtct
3	3121					
203		rtcccggagc	ctgaggcaga	tggcccaggg	caaggacccc	acagagtggc
	3181					
The second secon		gtgcgggctg	gccaacatgt	tegeetacea	cacgctgggc	tacgaggacc
And services	3241					
25		gcagaaggag	cctcagcctc	tggtctttgt	gatcgagctg	ctgcaggtgg
25	3301		~~ ~~ ~ ~ ~ ~ ~ ~	aasaasataa	242442424	aggaataat
		ggcagggctg	gagggctgtg	ccagcactgg	agagggacag	egggeaceac
	3361	agggagtag	aasataasas	ataggetatt	tatatttaa	taataccaca
	3421	accecactyy	ccactygaca	gegeeeegee	tctgtttaga	caacacgaga
30		accataggag	aatacqaatt	tgaaaaaaaa	gtcctctgat	ttttccacaa
30	3481	gecaegggag	aacacgaacc	egaaaaaaaa	900000940	333333333
		ttaatactaa	acataataac	ccacacctat	aatcctagca	ctttaaaaaa
	3541		3000330330			·
		tggatcacct	gaggtcagga	qttcqaaqac	cagcctggcc	aacatqqtaa
	- 5 - 5 5 5 5 5 6	55	5-55	5 5 5 5 5 5 5 5 5	5 55	23

	3601					
	aaccccgtct	ctattaaaaa	cacaaaaatt	aaccgggtgt	ggtggtgcat	gcctgtaatc
	3661					
	aatcccagct	acttgggaat	ttgaggcatg	agaattgctt	gaacctggaa	gtggaggttg
5	3721					
	cagtgagcag	agatcatgtc	agtgcatttt	aacctgggtg	acagagtgag	actccatgtc
	3781					
	caaaaaaaag	aaaaaaaaa	aaagtccact	tggaaccagt	ttttaaaaat	gtgattcatt
	3841					
10	ttcattgtgg	aggcatttta	tccacttcca	ctttcatttt	caggagttgg	agattataac
	3901					
	cgcctccttg	gttcctgtgg	tttgtgggtt	cagacttggt	tctctngtgg	cgggagaggc
	3961					
TO SUPPLY OF THE PARTY OF THE P	tgcatggaac	tccccacatc	ctcccaacca	ggagccccag	agtgattggc	agcgcgtgtt
15	4021					
15 In the line of		tgagagaggg	ttagggccag	ggtcaaggtc	aggtcaggac	tcagcttatg
THE STATE OF THE S	4081					
		aggctcagcc	tgagagctat	gtgggtgaat	aaaataaaat	aagaactgtg
\$B	4141				l a charle selection	
20		gccccttaca	ggcttgctgt	cacagttgtg	tggtctgtgc	actgcacaag
	4201			L - L		a+++aaa+aa
		atctcctcca	aggtgctcat	tatagacatt	gtatattggt	atticcataa
	4261		a a a a t a a t a t	2++ 2++ 2+ 22	annagaat	attaataaaa
25		ccagcagatg	guadiagigi	actycictaa	caaaacgagt	accegegaca
25	4321	tattagaagt	a a act at at t	astassaaa	caccttttcc	tagtttggag
	4381	caccagaage	gaagegeeee	gatgaatggg	caccecece	cageeegeae
		atttaggga	aaattttaa	cattattact	tctttccctt	atctatatac
	4441	acccagggca	333000033	cgccgccgcc		5000500050
30		caagcatgac	t.t.cagggaga	tataccacaa	ggtcctgttt	ttcagatctc
50	4501	caageaegae	cccagggaga		33	5555
		caggedeetg	agatecetae	ctcactgacc	tgcagctctg	qqqccaqqtt
	4561		555-35		J J -J	
		gtgattacca	gagggagacc	tggaacctga	gcaatcatga	gaagatgaag

	5641					
	aaaccgaggg	atgggggata	cagagaggtt	aaggatcatg	gcggggctga	gggtcttgga
	5701					
	ggctggtgag	tcccagctgg	gctggggctg	cctctgaggc	tgggaaggga	gctgtagctg
5	5761					
	gatgctccct	gctccccaca	ggcatcgtga	aggcctacta	cgtgcgtgcc	cgggctcacg
	5821					
	cagaggtgtg	gaatgaggcc	gaggccaagg	cggacctcca	gaaagtgctg	gagctggagc
	5881					
10	cgtccatgca	gaaggcggtg	cgcagggagc	ttgaggctgc	tggagaaccg	catggcggag
	5941					
	aacaggagga	ggagcggctg	cgctgccgga	acatgctgag	ccagggtgcc	acgcagcctc
	6001					
A COMMITTED TO THE COMM		acccacagag	ccacccgcac	agtcatccac	agagccacct	gcagagccac
15	6061					
10 10 10 10 10 10 10 10 10 10 10 10 10 1		atctgcagag	ctgtccgcag	ggccccctgc	agagccagcc	acagagccac
THE THE STATE OF T	6121					
		agggcactcg	ctgcagcact	gagccccctg	aggcccacag	ccacccagge
28	6181					
20		tggcctggtc	acttctggtt	cgattgacca	ggatcgtggt	gicactitit
	6241		~~~	tanananana	agatagtaaa	22222222
and A. Server		attaattitt	gadalCadag	Luayacacac	ccatggtaaa	aaaaaaaaaa
The state of the s	6301	assagat sas	assasaatts	taataaaa	tagttttctc	ctctacccct
25	6361	caayyytaca	gaagageeea	cgaacaaaag	tagttttctc	ccccacccc
23		ccataccata	attttaatta	accctattt	taattcttct	ggtagttttc
	6421	cegegeeaeg	geeeeuueeg	accongress		JJ • • · J • · · · ·
		agtaatctgt	ttaaatcaqt	ttctagattt	taccccatgt	caatgacaaa
	6481		· · · · · · · · · · · · · · · · ·	J	5	J
30		atqctctqat	cctttctcat	gcctgatacc	cctccctgtc	tccccatttt
	6541	3 3		•		
		atttgggggt	catctcggtg	atttttgtaa	ctttacgcag	gacacttaga
	6601	2		-		
		atcccactga	ctttagtggg	gtcttgatgt	agggtgggca	agccccgaca

```
5
```

15.

20=

25

30

```
(2) INFORMATION FOR SEQ ID NO:2:
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA Baboon
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
atqqatqccq ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc
acgggcgagc tcccaaactt catcaccgga tcccgagtga tctttcattt ccgcaccatg
aaatgtgatg aggagcgcac ggtcatcgac gacagccggc aggtggacca gcccatgcac
atcatcatcg ggaacatgtt caagetegag gtetgggaga teetgeteae etecatgagg
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg
tcccggagcc tgcggcagat ggcccagggc aaggacccca cggagtggca cgtgcacaca
tgcgggctgg ccaacatgtt cgcctaccac acactgggct acgaggacct ggacgagctg
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt
gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgtc
ctccacggag agggaaatcg gctcttcaag ctgggccgct acgaggaggc ctcttccaag
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc atgggaggtg
cagtggctga agctggagaa gatgatcaac accctgaccc tcaactactg ccagtgcctg
ctgaagaagg aggagtatta cgaggtgctg gagcacacca gtgacattct ccggcaccac
ccaggcatcg tgaaggccta ctatgtgcgt gcccgggctc acgcagaggt gtggaatgag
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccatccat gcagaaggcg
gtgcgcaggg agctgaggct gctggagaac cgcatggcag agaagcagga ggaggagcgg
ctgcgctgcc ggaacatgct gagccaggga gccacgcagc ctcccacaga gccaccggca
gagececaca cageaceace tgeggagetg tecaeaggge caectgeaga gecaecegea
```

gageteece tgteeceagg geacteactg cageactga

	(2) INFORMATION FOR SEQ ID NO:3:
	(i) SEQUENCE CHARACTERISTICS:
5	(A) LENGTH: bases
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA <i>Chimpansee</i>
10	(ix) FEATURE:
	(A) NAME/KEY: AIPL1 gene
	(B) LOCATION:
	(D) OTHER INFORMATION: produces aryl-hydrocarbon
e 1 1 handen de en verden de en	receptor interacting protein-like 1
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
tgtcc	geagdgcat.compostgatgatagtogaaagtgcaacccompostgaaccaacaggcattotgcagcaggcagcaggcagcccc
10 mm to 10	(2) INFORMATION FOR SEQ ID NO:4:
To the disperse	(i) SEQUENCE CHARACTERISTICS:
20=	(A) LENGTH: bases
2	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
(1 mg	
od od od wy (you)	(D) TOPOLOGY: linear
41 100g	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA <i>Cow</i>
25	
	(ii) MOLECULE TYPE: cDNA Cow
	(ii) MOLECULE TYPE: cDNA <i>Cow</i> (ix) FEATURE:
	<pre>(ii) MOLECULE TYPE: cDNA Cow (ix) FEATURE:</pre>
	<pre>(ii) MOLECULE TYPE: cDNA Cow (ix) FEATURE:</pre>

atggatgccactctgctcctgaatgtggaagggatcaagaaaaccattctgcatgggggcacagg ggacctccccaacttcattactggagcccgagtgacctttcatttccgaaccatgaaatgtgatg aggagcggacggtgatagacgacagcaagcaggtgggccatcccatgcacatcatcattgggaac atgttcaagctggaggtctgggagatcttgctgacgtccatgcgggtcagcgaggtggccgagtt

30

5

10

ttggtgcgacaccatccacacaggggtctaccccatcctgtcccggagcctgcggcagatggcgg agggtaaggaccccacagagtggcacgtgcacacgtgtggcttggccaacatgttcgcttaccac acgctgggctacgaggacctggacgagctgcagaaggagcctcagccactgatcttcataatcga gttgctgcaggtcgaggccccgagccagtaccagagggagacctggaacctgaataaccaggaga agatgcaggcggtgcccatcctccatggagaaggaaaccggctcttcaagctgggccgctacgag gaggcctccaacaagtaccaggaagccatcgtctgcctgaggaacctgcagaccaaggagaaacc ctgggaggtgcagtggctgaagctggagaagatgatcaacaccctgatcctgaactactgtcagt gtctgctgaagaaggaggagtactacgaggtgctggaacacactagtgacatcctccggcatcac ccaggcatcgtgaaggcctactatgtgagggcccgggctcacgccgaggtgtggaatgaggcgga agccaaggcggatctggagaaagtgctggagctgtgcatgcgtgcagaggcggtgcagaggg agctgaggctgctggagaaccggctggaggagaaacgcgaggaggagcgactgccggaac atgctgggctagtgcgcaggcgccaagcctcctgcctccgcccccgcycctccaccccccaa aaaaaaaaaaaaattttt

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Dog
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

tgtacgggggcaccggcgagctcccaaacttcctcacggggtcccgggtcatctttcacttccgcacaacgaaatgcgacgaggcgggacagtgatcgacgacagcaagcgtgtgggccatcccatgca $\verb|catcatcatcgggaacatgttcaagctggaggtctgggaggtgctgctgacatccatgcgcgtgg|\\$ gcgaggtggccgagttctggtgcgactctattcacacaggagtctaccccatcctgtcccggagc ctgcggcaggtggcggagggcaaggaccccactgagtggcatgtacacacgtgcggcttggccaa catgtttgcctatcacacgctgggctacgaggacctggacgagctacagaaggagccgcagcccc

30

5

10 (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA mouse
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

atggacgtctctctactcctcaatgtggagggtgtcaagaagaccattctgcatgggggacagg
agagctccccaacttcatcactggctccagagtgacctttcatttccgaacaatgaagtgtgatg
aagaacgcacggtgatcgatgacagcaagcaggtgggccagcccatgagcatcatcatcggcaac
atgttcaagctggaggtgtgggagacgctgctgacctccatgcggctgggcgaggtggctgagtt
ctggtgcgacaccattcacacaggggtctaccctatgttgtcccgcagtctgcggcaggtggctg
agggcaaggaccccacaagctggcatgtgcacacgtgcgggttggccaacatgtttgcataccac
acgctgggctacgaggacctggatgagctgcagaaagagccacagcctcttgtcttcctgtatga
actgttgcaggtggaggccccaaatgagtaccagagggagacgtggaacctgaataatgaagag
aggatgcaggcggtacctcttcttcatggagaaggcaacaggctctacaagctgggacgctatgat
caggccgccaccaagtaccaggaggccattgtgtgcctgaggaaccttcagaccaaggagagacc
ctgggaggttgagtggctgaagctggagaagatgatcaacaccctgatcctcaactactgccagt
gcctgctgaagaagaggaggagtactacgaggtgttggagcacaccagcgacattctacgacaccac

30

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Rhesus monkey
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Squirrel monkey
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

atggatgccgctctgctcctgaacgtggaagggtcaagaagaccattctgcacgggggcacggg cgagctcccaaatttcatcaccggatcccgagtgatctttcatttccgcaccatgaaatgtgatg aggagcggacggtgattgacgacagcagggaggtgggccagcccatgcacatcatcatcgggaac $\verb|atgttcaagctggaggtctgggagatcctgctcacgtccatgcgggtgcgagaggtggccgagtt|\\$ ctggtgcgacaccatccacacgggggtctaccccatcctgtcccggagcctgcggcagatggccc agggcaaggacccgacggagtggcatgtgcacacgtgcgggctggccaacatgttcgcctaccac $\verb|acgctgggctacgaggacctggatgagctgcagaaggagcctcagcctctgatctttgtgatcga|\\$ gctgctgcaggttgatgccccaagtgattaccagagggagacctggaacctgagcaatcacgaga agatgaaggtggtgcccgtcctccatggagaaggaaataggctcttcaagctgggccgctacgag gaggcctcttccaagtaccaggaggccatcatctgcctaaggaacctgcagaccaaggagaaacc ctgggaggtgcagtggctgaagctggagaagatgatcaataccctgatcctcaactactgtcagt $\verb|gtctgctgaagaaggaggagtactacgaggtcctggagcataccagtgacattctccggcaccac|$ ccaggcattgtgaaggcctactatgtgcgcgcccgggctcacgcggaggtgtggaacgaggccga ggccaaggcggacctccagaaagtgctggagctggagccgtccatgcagaaggcggtgcgcaggg agetgaggetgetggagaaccgcatggcggagaagcaggaggaggagcggctgcgctaac atqctgagccagggggccacgtggtcccccgcggagccacccgcagagccacctgcagagtcatc

	(2) INFORMATION FOR SEQ ID NO:9:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 15 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Met79Thr Mutation	
	(B) LOCATION: 7781	
A 1 a Tables OF The Tables To To To Tables To Tables	(D) OTHER INFORMATION: Thr 79 mutation	
15 mg may man	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
7.5 September 1.5 September 1.	acc tcc acg cgg gtg	15
AN INC.	Thr	
The state of the s		
21, 21, 1995	(2) INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
20 miles of the second of the	(A) LENGTH: 15 bases	
01 2000 1000 1000 1000 1000 1000 1000 10	(B) TYPE: nucleic acid	
Services	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Trp88X mutation	
	(B) LOCATION: 8690	
	(D) OTHER INFORMATION:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	gag ttc tga tgc gac	15
	X	

Page 90

(2) INFORMATION FOR SEQ ID NO:11:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(A) NAME/KEY: AIPL1 Ala197Pro mutation

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

Page 94

15

15

	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Ala336del2 mutation	
	(B) LOCATION:	
5	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
	t ccc gca gcc acc	13
	del AG	
10	(2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
20 ftm; 5 72 cm²	(C) STRANDEDNESS: single	
15 The last line and the other	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Cys42X mutation	
TO A STANDARD AND AND AND AND AND AND AND AND AND AN	(B) LOCATION:	
	(D) OTHER INFORMATION:	
20-1	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
	atg aaa tga gat gag	15
THE ROOF	X	
25	(2) INFORMATION FOR SEQ ID NO:24:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Leu257del9 mutation	
	(B) LOCATION:	

	(2) INFORMATION FOR SEQ ID NO:27:
	(i) SEQUENCE CHARACTERISTICS:
5	(A) LENGTH: 20 bases
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
10	(ix) FEATURE:
	(A) NAME/KEY: AIPL1 IVS2+66G->C Benign
	Variants/Polymorphisms
	(B) LOCATION:
And September 1 Comments of the Comments of th	(D) OTHER INFORMATION:
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
AND STATE OF THE PARTY OF THE P	TTT GCC GGG CTG
	G->C
To a security 1 to S	
or the comptent of the compten	(2) INFORMATION FOR SEQ ID NO:28:
203	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 20 bases
To the state of th	(B) TYPE: nucleic acid
See Marie	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: DNA (genomic)
	(ix) FEATURE:
	(A) NAME/KEY: AIPL1 IVS2-88C->T Benign
	Variants/Polymorphisms
	(B) LOCATION:
30	(D) OTHER INFORMATION:
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
	TCC TCT CAG GAG

C->T

5

10

- (2) INFORMATION FOR SEQ ID NO:29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: NAME/KEY: Benign IVS2-14G->A (A) AIPL1 Variants/Polymorphisms (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: ATC CAT TTA TCC G->A (2) INFORMATION FOR SEQ ID NO:30: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS2-10A->C Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGT TTC TCC CCA

A->C

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:

Page 99

(A) LENGTH: 20 bases

(B) TYPE: nucleic acid

30

5

10

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS5+18G->A Benign

Variants/Polymorphisms

- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGG AGC GGA CAG

G - > A

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 Asp90His Benign

Variants/Polymorphisms

- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGG TGC CAC ACC

His

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

Page 101

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

	AGT GAC ATT CTC	
	Asp	
5	(2) INFORMATION FOR SEQ ID NO:42:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 primer	
11 mm, 2	(B) LOCATION:	
15	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
A STATE OF THE PARTY OF T	5'-AAGAAAACCATTCTGCACGG-3'	20
yes broken yes broken of magain of magain to the of the of the the of the of th		
50 50	(2) INFORMATION FOR SEQ ID NO:43:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 19 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
ŧ	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 primer	
	(B) LOCATION:	
	(D) OTHER INFORMATION:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
	5'-TGCAGCTCGTCCAGGTCCT-3'	19
	(2) INFORMATION FOR SEQ ID NO:44:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site 5 (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51: 35 cagagtgcaccgtctcggtgactagGTGATCTTTC 10 (2) INFORMATION FOR SEQ ID NO:52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52: CSACACCATCgtaagtaggccctgcgcgcctgtct 35 (2) INFORMATION FOR SEQ ID NO:53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid 30 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: NAME/KEY: AIPL1 gene exon/intron Acceptor

(D) TOPOLOGY: linear

(B) LOCATION: 17p13.1 (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: 5 gccatccatccgtttatccccacagCACACGGGGG (2) INFORMATION FOR SEQ ID NO:54: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases 10 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: 20 GCTGCTGCAGgtggggctggggttggcagggctgg (2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6689 bases 25 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: 30 (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site (B) LOCATION:

splice site

Page 110

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

35

35

30

5

10

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

 GCAGACCAAGgtcagaggccgctggccacggggtg 35
- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

 catggctgaccttctccctgggcagGAGAAGCCRT 35
- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:

Page 111

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	5'-gggccttgaacagtgtgtct-3'	20
	(2) INFORMATION FOR SEQ ID NO:63:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 19 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 gene Exon 2 Primer	
	(B) LOCATION: 297	
12) - September 1 - September	(D) OTHER INFORMATION:	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
177 COM 277 COM 278 CO	5'-tttcccgaaacacagcagc-3'	19
	(2) INFORMATION FOR SEQ ID NO:64:	
W MAN	(i) SEQUENCE CHARACTERISTICS:	
20_	(A) LENGTH: 18 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA Primer	
25	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 gene Exon 3 Primer	
	(B) LOCATION: 364	
	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
30	5'-agtgagggagcaggattc-3'	18
	(2) INFORMATION FOR SEQ ID NO:65:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	

(A) NAME/KEY: AIPL1 gene Exon 4 Primer

(2) INFORMATION FOR SEQ ID NO:70:

30

- (A) NAME/KEY: Human Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
- 5 MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDE
 ERTVIDDSRQVGQPMHIIIGNMFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSR
 SLRQMAQGKDPTEWHVHTCGLANMFAYHTLGYEDLDELQKEPQPLVFVIELLQVDAPS
 DYQRETWNLSNHEKMKAVPVLHGEGNRLFKLGRYEEASSKYQEAIICLRNLQTKEKPW
 EVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHHPGIVKAYYVRARAHAE
 VWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLXCRNMLSQGATQP
 PAEPPTEPPAOSSTEPPAEPPTAPSAELSAGPPAEPATEPPPSPGHSLQH
 - (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Chimpansee Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEOUENCE DESCRIPTION: SEQ ID NO:73:
 - MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVGQPMHIIIGN
 MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH
 TLGYEDLDELQKEPQPLVFVIELLQVDAPSDYQRETWNLSNHEKMKAVPVLHGEGNRLFKLGRYE
 EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH
 PGIVKAYYVRARAHAEVWNEAEAKADLRKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN
 MLSQGATQPPAEPPTEPPAQSSTEPPAEPPPAPSAELSAGPPAETATEPPPSPGHSLQH
 - (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid

Page 118

(ix) FEATURE:

- (A) NAME/KEY: Baboon Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVDQPMHIIIGN MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH TLGYEDLDELQKEPQPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLTLNYCQCLLKKEEYYEVLEHTSDILRHH PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN MLSQGATQPPTEPPAEPHTAPPAELSTGPPAEPPAELPLSPGHSLQH

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Cow Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

MDATLLLNVEGIKKTILHGGTGDLPNFITGARVTFHFRTMKCDEERTVIDDSKQVGHPMHIIIGN MFKLEVWEILLTSMRVSEVAEFWCDTIHTGVYPILSRSLRQMAEGKDPTEWHVHTCGLANMFAYH TLGYEDLDELQKEPQPLIFIIELLQVEAPSQYQRETWNLNNQEKMQAVPILHGEGNRLFKLGRYE EASNKYQEAIVCLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH PGIVKAYYVRARAHAEVWNEAEAKADLEKVLELEPSMRKAVQRELRLLENRLEEKREEERLRCRN MLG

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids

Page 119

30

25

20

5

10

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:

10

25

30

- (A) NAME/KEY: Mouse Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

MDVSLLLNVEGVKKTILHGGTGELPNFITGSRVTFHFRTMKCDEERTVIDDSKQVGQPMSIIIGN
MFKLEVWETLLTSMRLGEVAEFWCDTIHTGVYPMLSRSLRQVAEGKDPTSWHVHTCGLANMFAYH
TLGYEDLDELQKEPQPLVFLYELLQVEAPNEYQRETWNLNNEERMQAVPLLHGEGNRLYKLGRYD
QAATKYQEAIVCLRNLQTKEKPWEVEWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH
PGIVKAYYMRARAHAEVWNAEEAKADLEKVLELEPSMRKAVLRELRLLESRLADKQEEERQRCRS
MLG

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Rhesus Monkey Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVDQPMHIIIGN
MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH
TLGYEDLDELQKEPQPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE
EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLTLNYCQCLLKKEEYYEVLEHTSDILRHH
PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN
MLSQGATQPPAEPPAQPPTAPPAELSTGPPADPPAEPPTAPPAELSTGPPAEPPAELPLSPGHSLQH

(2) INFORMATION FOR SEQ ID NO:78:

Page 120

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Squirrel Monkey Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSREVGQPMHIIIGN
MFKLEVWEILLTSMRVREVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH
TLGYEDLDELQKEPQPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE
EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH
PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN
MLSQGATWSPAEPPAEPPAESSTEPPAEPPAEPPAELTLTPGHPLQH